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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/263,626

DATE: 03/25/1999  
TIME: 18:29:23

Input Set: I263626.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: Moore, Paul A.  
2 Rosen, Craig A.  
3 Ruben, Steven M.  
4 <120> TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like  
5 <130> FILE REFERENCE: PF466  
6 <140> CURRENT APPLICATION NUMBER: US/09/263,626  
7 <141> CURRENT FILING DATE: 1999-03-05  
8 <150> EARLIER APPLICATION NUMBER: 60/086,505  
9 <151> EARLIER FILING DATE: 1998-05-22  
10 <150> EARLIER APPLICATION NUMBER: 60/078,563  
11 <151> EARLIER FILING DATE: 1998-03-19  
12 <160> NUMBER OF SEQ ID NOS: 30  
13 <170> SOFTWARE: PatentIn Ver. 2.0  
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15 <211> LENGTH: 1573  
16 <212> TYPE: DNA  
17 <213> ORGANISM: Homo sapiens  
18 <220> FEATURE:  
19 <221> NAME/KEY: CDS  
20 <222> LOCATION: (13)..(1125)  
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23 Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe  
24 1 5 10  
25 ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga 99  
26 Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly  
27 15 20 25  
28 gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147  
29 Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr  
30 30 35 40 45  
31 tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195  
32 Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg  
33 50 55 60  
34 ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag 243  
35 Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln  
36 65 70 75  
37 gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac 291  
38 Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp  
39 80 85 90  
40 att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca 339  
41 Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala  
42 95 100 105  
43 agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg 387  
44 Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val

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45	110	115	120	125	
46	aga ttt tgc tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg				435
47	Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu				
48		130	135	140	
49	tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac				483
50	Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp				
51		145	150	155	
52	acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa				531
53	Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu				
54		160	165	170	
55	ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct				579
56	Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala				
57		175	180	185	
58	atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag				627
59	Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu				
60		190	195	200	205
61	gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca				675
62	Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr				
63		210	215	220	
64	cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc				723
65	Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser				
66		225	230	235	
67	ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa				771
68	Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys				
69		240	245	250	
70	tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa				819
71	Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys				
72		255	260	265	
73	tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag				867
74	Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu				
75		270	275	280	285
76	tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt				915
77	Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly				
78		290	295	300	
79	gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc				963
80	Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala				
81		305	310	315	
82	aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag				1011
83	Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu				
84		320	325	330	
85	aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa				1059
86	Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln				
87		335	340	345	
88	ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac				1107
89	Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp				
90		350	355	360	365
91	cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt				1155
92	Arg Ser Tyr Val Ala Leu				
93		370			
94	caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccacat				1215

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95      ggatgggaag tctccacgcc aatgatggta ggactaggag actctgaaga cccagcctca 1275
96      cgcctaatag cggccactgc cctgctaact ttccccaca tgagtctctg tgttcaaagg 1335
97      cttgatggca gatgggagcc aattgctcca ggagatttac tcccagttcc ttttcgtgcc 1395
98      tgaacgttgt cacataaacc ccaaggcagc acgtccaaaa tgctgtaaaa ccattctccc 1455
99      actctgtgag tccccagttc cgtccatgta cctgttccat agcattggat tctcggagga 1515
100     ttttttgtct gttttgagac tccaaaccac ctctaccctt acaaaaaaaaa aaaaaaaa 1573
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102     <211> LENGTH: 371
103     <212> TYPE: PRT
104     <213> ORGANISM: Homo sapiens
105     <400> SEQUENCE: 2
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108     Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile
109           20             25             30
110     Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala
111           35             40             45
112     Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly
113           50             55             60
114     Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His
115           65             70             75             80
116     Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr
117           85             90             95
118     Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp
119           100            105            110
120     Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser
121           115            120            125
122     Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly
123           130            135            140
124     Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp
125           145            150            155            160
126     Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp
127           165            170            175
128     Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp
129           180            185            190
130     Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys
131           195            200            205
132     Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro
133           210            215            220
134     Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile
135           225            230            235            240
136     Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg
137           245            250            255
138     Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe
139           260            265            270
140     Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr
141           275            280            285
142     Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln
143           290            295            300
144     Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu

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145      305      310      315      320
146      Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala
147      325      330      335
148      Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp
149      340      345      350
150      Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr
151      355      360      365
152      Val Ala Leu
153      370
154      <210> SEQ ID NO 3
155      <211> LENGTH: 363
156      <212> TYPE: PRT
157      <213> ORGANISM: Homo sapiens
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161      Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Gly Asp Phe Phe Leu
162      20      25      30
163      Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro
164      35      40      45
165      Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp
166      50      55      60
167      Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly
168      65      70      75      80
169      Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr
170      85      90      95
171      Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu
172      100      105      110
173      Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu
174      115      120      125
175      His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile
176      130      135      140
177      Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln
178      145      150      155      160
179      Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His
180      165      170      175
181      Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser
182      180      185      190
183      Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys
184      195      200      205
185      Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser
186      210      215      220
187      Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn
188      225      230      235      240
189      Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala
190      245      250      255
191      Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser
192      260      265      270
193      Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro
194      275      280      285

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195      Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe
196          290                      295                      300
197      Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro
198          305                      310                      315                      320
199      Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly
200          325                      330                      335
201      Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp
202          340                      345                      350
203      Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro
204          355                      360
205      <210> SEQ ID NO 4
206      <211> LENGTH: 733
207      <212> TYPE: DNA
208      <213> ORGANISM: Homo sapiens
209      <400> SEQUENCE: 4
210      gggatccgga gcccaaactct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60
211      aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120
212      tctcccgga ctcctgaggtc acatgcgtgg tggaggacgt aagccacgaa gaccctgagg 180
213      tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
214      aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
215      ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
216      agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
217      catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct 480
218      atccaagcga catcgccgtg gagggtggaga gcaatgggca gccggagaac aactacaaga 540
219      ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600
220      acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctg 660
221      acaaccacta cagcgagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
222      gactctagag gat
223      <210> SEQ ID NO 5
224      <211> LENGTH: 5
225      <212> TYPE: PRT
226      <213> ORGANISM: Homo sapiens
227      <220> FEATURE:
228      <221> NAME/KEY: SITE
229      <222> LOCATION: (3)
230      <223> OTHER INFORMATION: Xaa equals any amino acid
231      <400> SEQUENCE: 5

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w--> 232 Trp Ser Xaa Trp Ser  
233 1 5

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234      <210> SEQ ID NO 6
235      <211> LENGTH: 86
236      <212> TYPE: DNA
237      <213> ORGANISM: Homo sapiens
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240      cccgaaatat ctgccatctc aattag
241      <210> SEQ ID NO 7
242      <211> LENGTH: 27
243      <212> TYPE: DNA
244      ORGANISM: Homo sapiens

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## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I263626.RAW

Line	?	Error/Warning	Original Text
232	W	"N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser
337	W	"N" or "Xaa" used: Feature required	Xaa Xaa Trp Xaa Xaa Trp Ser
352	W	"N" or "Xaa" used: Feature required	Thr Xaa Pro Ser Xaa Trp Ser
375	W	"N" or "Xaa" used: Feature required	Trp Xaa Xaa Xaa Pro Xaa Pro
386	W	"N" or "Xaa" used: Feature required	Ile Pro Xaa Val Pro Asp Pro
451	W	"N" or "Xaa" used: Feature required	Leu Trp Arg Xaa Lys Lys Phe Leu Xaa Pro S
453	W	"N" or "Xaa" used: Feature required	Ser Ile Phe Pro Gly Leu Phe Xaa Ile His G
501	W	"N" or "Xaa" used: Feature required	ctcmytccca gcgtgccaga cccgaaatcc atcttccc
542	W	"N" or "Xaa" used: Feature required	Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln A
548	W	"N" or "Xaa" used: Feature required	Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa T
575	W	"N" or "Xaa" used: Feature required	Trp Xaa Trp Ser

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PREVIOUSLY ERRORED SEQUENCES-EDITED

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1	<210>	30
2	<211>	4
3	<212>	PRT
4	<213>	Homo sapiens
5	<220>	
6	<221>	SITE
7	<222>	(2)
8	<223>	Xaa equals any amino acid
9	<400>	30
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